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(54) Title: ITERATIVE RESEQUENCING

(57) Abstract

The invention provides iterative methods of analyzing a target nucleic acid that represents a variant of a reference nucleic acid. An array of probes is designed to be complementary to an estimated sequence of a target nucleic acid. The array of probes is then hybridized to the target nucleic acid. The target sequence is reestimated from hybridization pattern of the array to the target nucleic acid. A further array of probes is then designed to be complementary to the reestimated sequence, and this array is used to obtain a further reestimate of the sequence of the target nucleic acid. By performing iterative cycles of array design and target sequence estimation, the estimated sequence of the target converges with the true sequence.